```
                                                    *
Heps   RIVGGRDTSL GRWPWQVSL. ....RYDG.A HLCGGSLLSG DWVLTAAHCF PE....RNRV LSRWRVFAGA VAQASPHGLQ
Tadg15 RVVGGTDADE GEWPWQVSL. ....HALGQG HICGASLISP NWLVSAAHCY IDDRGFRYSD PTQWTAFLGL HDQSQRSAPG
Scce   KIIDGAPCAR GSHPWQVAL. ....LSGNQL H.CGGVLVNE RWVLTAAHC. .........K MNEYTVHLGS DTLG..DR.R
Try    KIVGGYNCEE NSVPYQVSL. ....NSGYHF ..CGGSLINE QWVVSAGHC. .........Y KSRIQVRLGE HNIEVLEG.N
Chymb  RIVNGEDAVP GSWPWQVSL. ....QDKTGF HFCGGSLISE DWVVTAAHC. ........GV RTSDVVVAGE FDQGSDEE.N
Fac7   RIVGGKVCPK GECPWQVLL. ....LVNG.A QLCGGTLINT IWVVSAAHCF DKIKNWRNLI .....AVLGE HDLSEHDGDE
Tpa    RIKGGLFADI ASHPWQAAIF AKHRRSPGER FLCGGILISS CWILSAAHCF QERFPPHHL. ....TVILGR .TYRVVPGEE

                                  *
Heps   LGVQAVVYHG GYLPFRDPNS EENSNDIALV HLSS.PLPLT EYIQPVCLPA ...AGQALVD GKICTVTGWG NTQYYGQQ.A
Tadg15 VQERRLKRII SHPFFNDFTF D...YDIALL ELEK.PAEYS SMVRPICLPD ...ASHVFPA GKAIWVTGWG HTQYGGTG.A
Scce   AQRIKASKSF RHPGYSTQT. ..HVNDLMLV KLNS.QARLS SMVKKVRLPS ...RCE..PP GTTCTVSGWG TTTSPDVTFP
Try    EQFINAAKII RHPQYDRKT. ..LNNDIMLI KLSS.RAVIN ARVSTISLPT ...APP..AT GTKCLISGWG NTASSGADYP
Chymb  IQVLKIAKVF KNPKFSILT. ..VNNDITLL KLAT.PARFS QTVSAVCLPS ...ADDDFPA GTLCATTGWG KTKYNANKTP
Fac7   QSRRVAQVII P....STYVP GTTNHDIALL RLHQ.PVVLT DHVVPLCLPE RTFSERTLAF VRFSLVSGWG QLLDRGATAL
Tpa    EQKFEVEKYI VHKEFDDDTY D...NDIALL QLKSDSSRCA QESSVVRTVC LPPADLQLPD WTECELSGYG KHEALSPFYS

                                                  *
Heps   GVLQEARVPI ISNDVCNGAD FYGN..QIKP KMFCAGYPEG G......IDA CQGDSGGPFV CEDSISRTPR WRLCGIVSWG
Tadg15 LILQKGEIRV INQTTCE..N LLPQ..QITP RMMCVGFLSG G......VDS CQGDSGGPL. ..SSVEADGR IFQAGVVSWG
Scce   SDLMCVDVKL ISPQDCTKV. .YKD..LLEN SMLCAGIPDS K......KNA CNGDSGGPLV C....R.... GTLQGLVSWG
Try    DELQCLDAPV LSQAKCEAS. .YPG..KITS NMFCVGFLEG G......KDS CQGDSGGPVV C....N.... GQLQGVVSWG
Chymb  DKLQQAALPL LSNAECKKS. .WGR..RITD VMICAG..AS G......VSS CMGDSGGPLV C....QKDGA WTLVGIVSWG
Fac7   ELMVLNVPRL MTQDCLQQSR KVGDSPNITE YMFCAGYSDG S......KDS CKGDSGGP.. ..HATHYRGT WYLTGIVSWG
Tpa    ERLKEAHVRL YPSSRCTSQH LLNRT..VTD NMLCAGDTRS GGPQANLHDA CQGDSGGPLV CLN..\.DGR MTLVGIISWG

                                                                    (SEQ ID NO.3)
Heps   T.GCALAQKP GVYTKVSDFR EWIFQAIKTH SEASGMVTQL ~~~~~~~~~~ ~~ 1 (SEQ ID NO:2)
Tadg15 D.GCAQRNKP GVYTRLPLFR DWIKENTGV~ ~~~~~~~~~~ ~~ 1 (SEQ ID NO:4)
Scce   TFPCGQPNDP GVYTQVCKFT KWINDTMKKH R~~~~~~~~~ ~~ 1 (SEQ ID NO:5)
Try    D.GCAQKNKP GVYTKVYNYV KWIKNTIAAN S~~~~~~~~~ ~~ 1 (SEQ ID NO:6)
Chymb  SDTCS.TSSP GVYARVTKLI PWVQKILAAN ~~~~~~~~~~ ~~ 1 (SEQ ID NO:7)
Fac7   Q.GCATVGHF GVYTRVSQYI EWLQKLMRSE PRPGVLLRAP FP 1 (SEQ ID NO:8)
Tpa    .LGCGQKDVP GVYTKVTNYL DWIRDNMRP~ ~~~~~~~~~~ ~~ 1
```

FIGURE 1

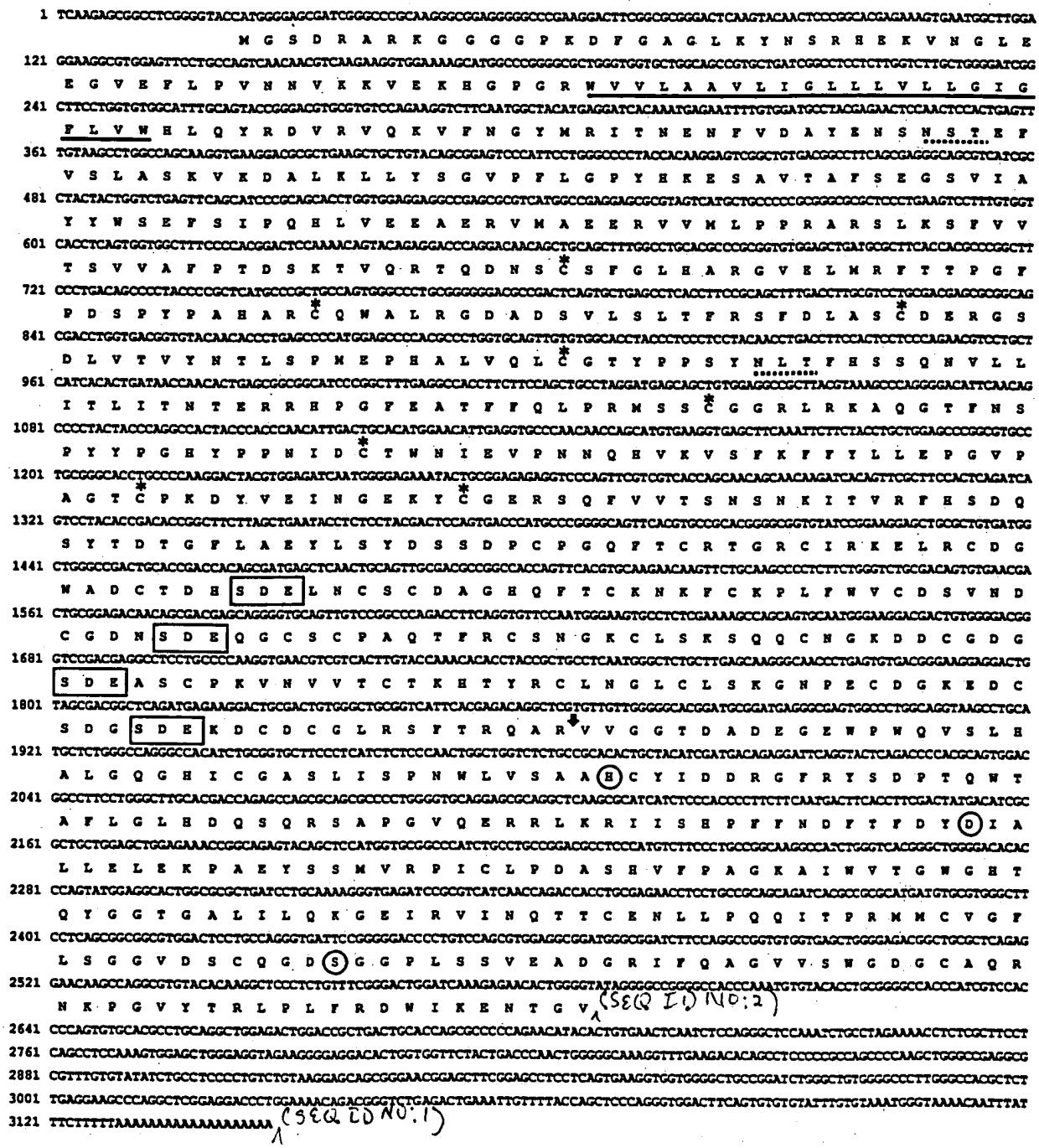


FIGURE 2

```
  1 MGSDRARKGG GGPKDFGAGL KYNSRHEKVN GLEEGVEFLP VNNVKKVEKH   1
 51 GPGRWVVLAA VLIGLLLVLL GIGFLVWHLQ YRDVRVQKVF NGYMRITNEN   2
101 FVDAYENSNS TEFVSLASKV KDALKLLYSG VPFLGPYHKE SAVTAFSEGS
151 VIAYYWSEFS IPQHLVEEAE RVMAEERVVM LPPRARSLKS FVVTSVVAFP
201 TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA HARCQWALRG
251 DADSVLSLTF RSFDLASCDE RGSDLVTVYN TLSPMEPHAL VQLCGTYPPS
301 YNLTFHSSQN VLLITLITNT ERRHPGFEAT FFQLPRMSSC GGRLRKAQGT   3
351 FNSPYYPGHY PPNIDCTWNI EVPNNQHVKV SFKFFYLLEP GVPAGTCPKD
401 YVEINGEKYC GERSQFVVTS NSNKITVRFH SDQSYTDTGF LAEYLSYDSS
451 DPCPGQFTCR TGRCIRKELR CDGWADCTDH SDELNCSCDA GHQFTCKNKF
501 CKPLFWVCDS VNDCGDNSDE QGCSCPAQTF RCSNGKCLSK SQQCNGKDDC   4
551 GDGSDEASCP KVNVVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSDEK
601 DCDCGLRSFT RQARVVGGTD ADEGEWPWQV SLHALGQGHI CGASLISPNW
651 LVSAAHCYID DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH
701 PFFNDFTFDY DIALLELEKP AEYSSMVRPI CLPDASHVFP AGKAIWVTGW   5
751 GHTQYGGTGA LILQKGEIRV INQTTCENLL PQQITPRMMC VGFLSGGVDS
801 CQGDSGGPLS SVEADGRIFQ AGVVSWGDGC AQRNKPGVYT RLPLFRDWIK
851 ENTGV SEQ ID NO:2
```

* : Conserved cysteine residue
NXT : Possible N-linked glycosylation site
SDE : Conserved SDE motif
▼ : Potential cleavage site
O : Conserved amino acids of catalytic triad H, D, S

1. Cytoplasmic domain
2. Transmembrane domain
3. CUB repeat
4. Ligand-binding repeat (class A motif) of LDL receptor like domain
5. Serine protease

FIGURE 3

6602OT ET2T2h6O

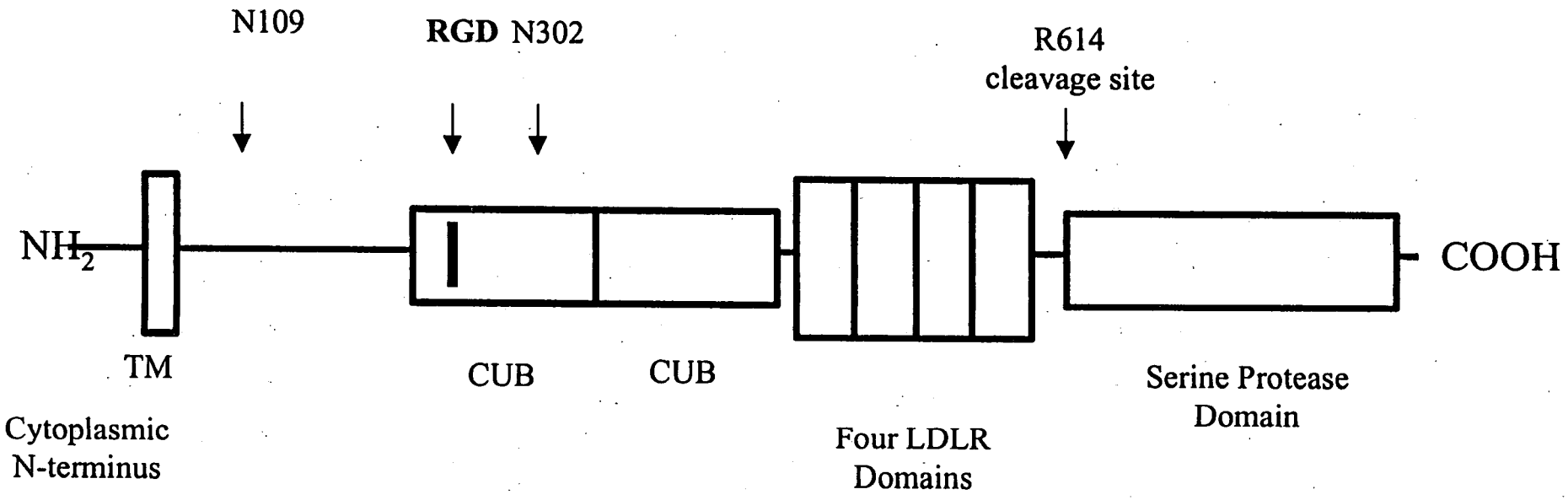


FIGURE 4

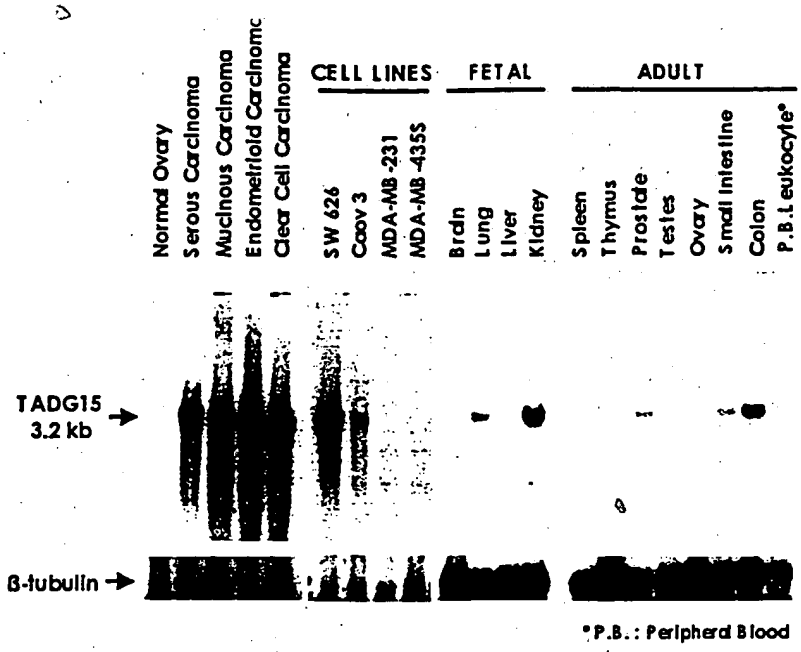
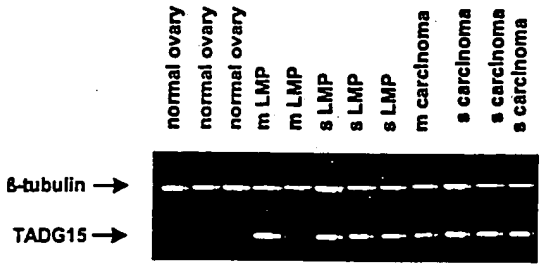

Normal Ovary
Serous Carcinoma
Mucinous Carcinoma
Endometrioid Carcinoma
Clear Cell Carcinoma
CELL LINES
SW 626
Caov 3
MDA-MB-231
MDA-MB-435
FETAL
Brain
Lung
Liver
Kidney
ADULT
Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
P.B.Leukocyte*
TADG15
3.2 kb
β-tubulin
*P.B.: Peripheral Blood

FIGURE 5

A


normal ovary
normal ovary
normal ovary
m LMP
m LMP
s LMP
s LMP
s LMP
m carcinoma
s carcinoma
s carcinoma
s carcinoma
β-tubulin
TADG15

B

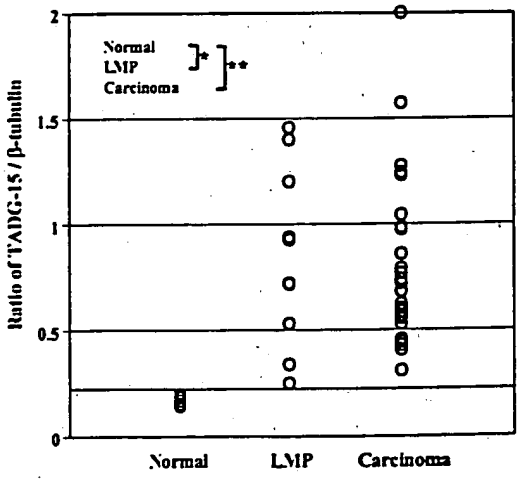

Normal
LMP
Carcinoma
*
**
Ratio of TADG-15 / β-tubulin
2
1.5
1
0.5
0
Normal
LMP
Carcinoma

FIGURE 6

6602017 ET2F2h60

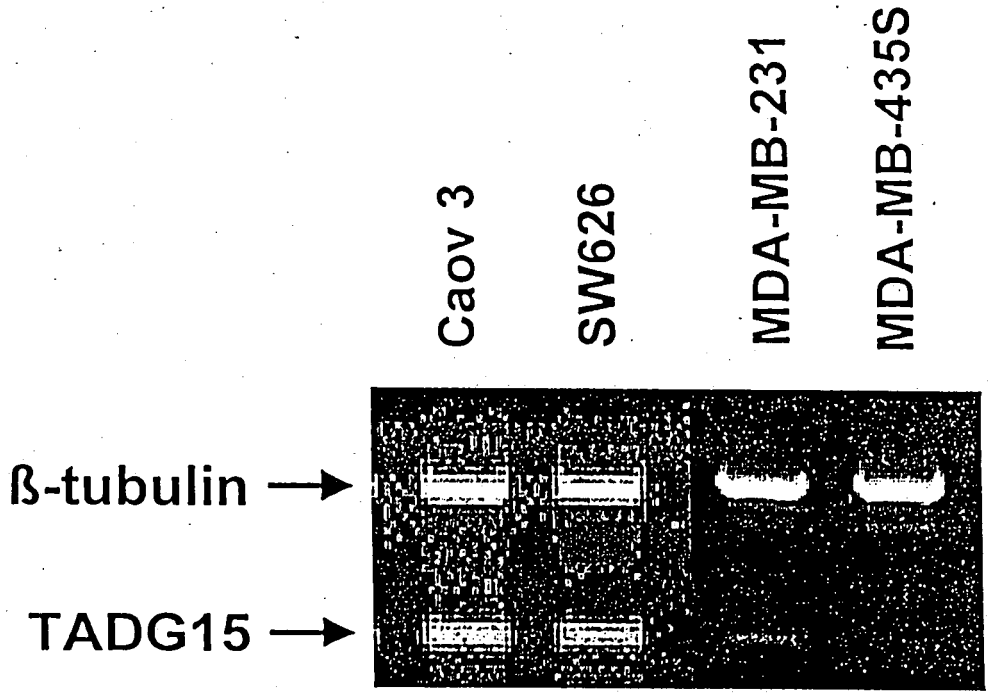


FIGURE 1

660201 "EP2T2160

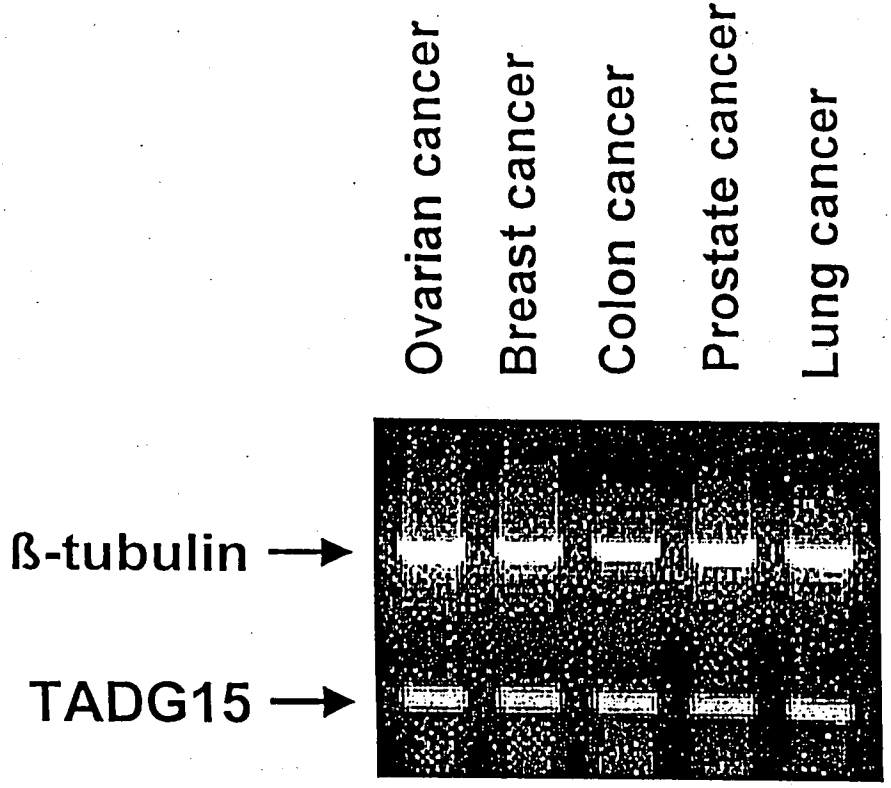


FIGURE 8

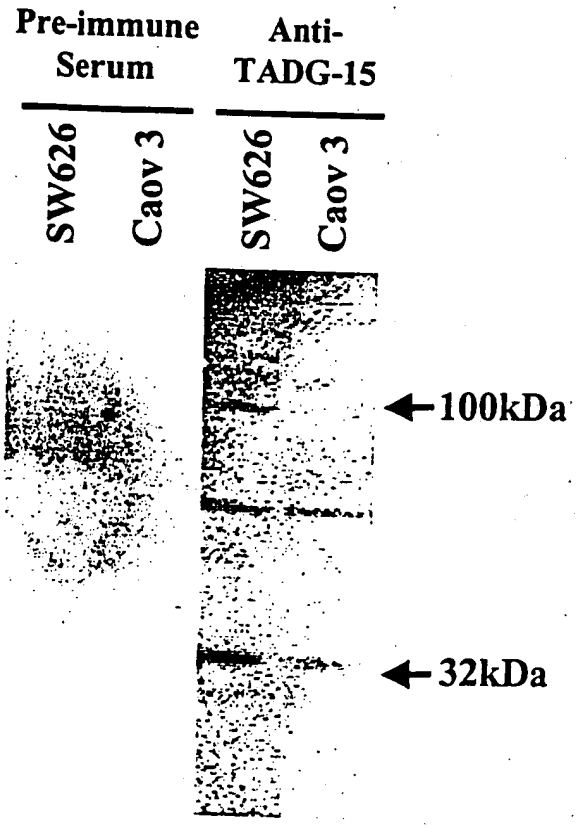

Pre-immune Serum
Anti-TADG-15
SW626
Caov 3
SW626
Caov 3
100kDa
32kDa

FIGURE 9

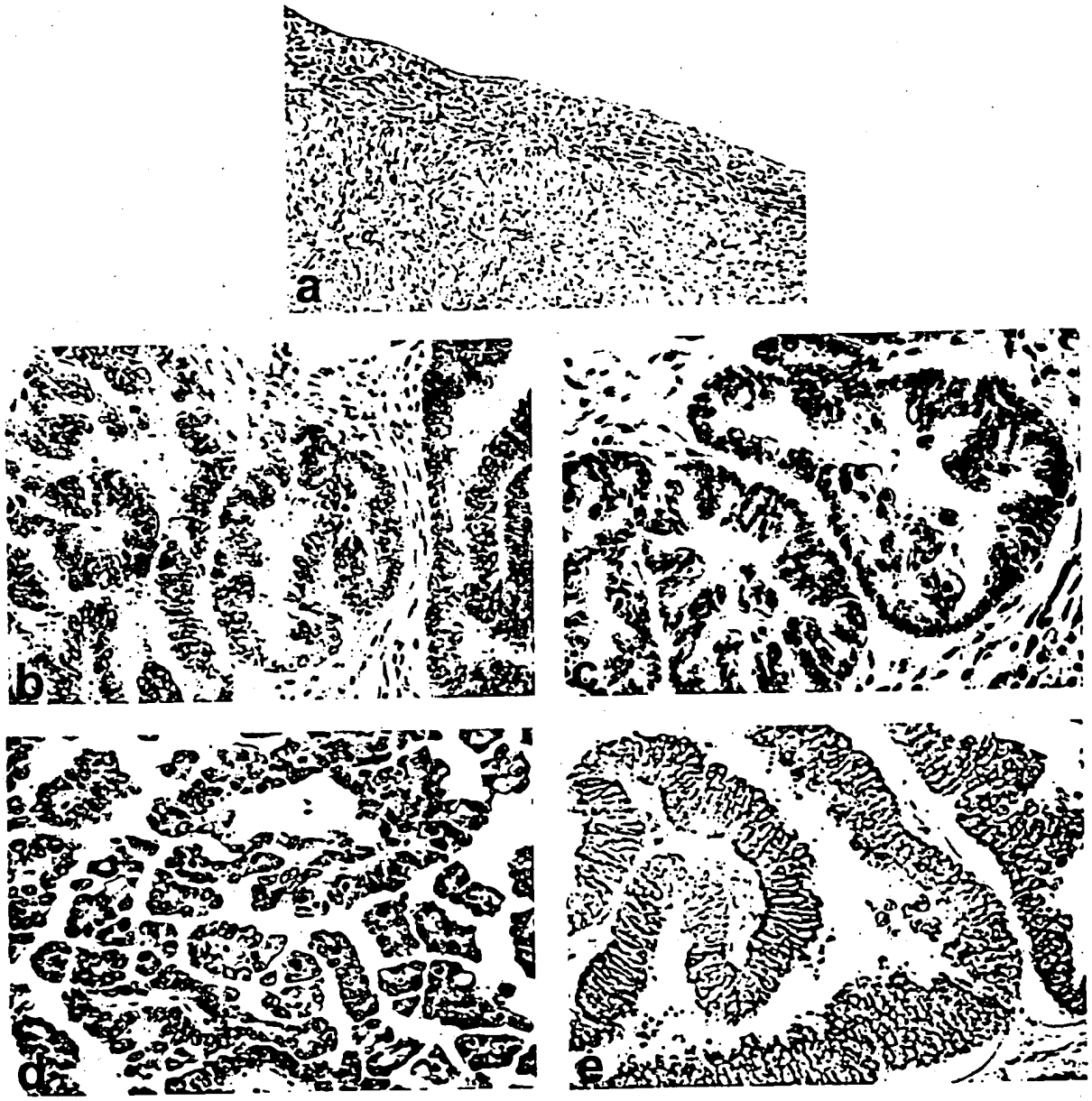


FIGURE 10

```
hTADG15  MGSDRARKGG [redacted]RDFGAGL KYNSRHEKVN GLEEGVEFLF VNNVKKVEKH  50
mEpithin ---N-G--A- --SQ------ --D--L-NM- -F-------- A--A-----R

hTADG15  GPGRWVVLAA VLIGLLLVLL GIGFLVWHLQ YRDVRVQKVF NGYMRITNEN 100
mEpithin --R-----V- --FSF--LS- MA-L----FH --N------- --HL-----I

hTADG15  FVDAYENSNS TEFVSLASKV KDALKLLYSG VPFLGPYHKE SAVTAFSEGS 150
mEpithin -L------T- ---I----Q- -E------NE --V------K ----------

hTADG15  VIAYYWSEFS IPQHLVEEAE RVMAEERVVM LPPRARSLKS FVVTSVVAFP 200
mEpithin ---------- --P--A--VD -A--V----T ------A--- --L-------

hTADG15  TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA HARCQWALRG 250
mEpithin I-PRML---- ------A--- H-AAVT---- ----N----- ------V---

hTADG15  DADSVLSLTF RSFDLASCDE RGSDLVTVYN TLSPMEPHAL VQLCGTYPPS 300
mEpithin ---------- ----V-P--- H--------D S--------V -R----FS--

hTADG15  YNLTFHSSQN VLLITLITNT ERRHPGFEAT FFQLPRMSSC GGRLRKAQGT 350
mEpithin -----L---- -F-V------ G---L----- -----K---- --V-SDT---

hTADG15  FNSPYYPGHY PPNIDCTWNI EVPNNQHVKV SFKFFYLLEP GVPAGTCPKD 400
mEpithin -S-------- ----N----- K----RN--- R--L---VD- N--V-S-T--

hTADG15  YVEINGEKYC GERSQFVVTS NSNKITVRFH SDQSYTDTGF LAEYLSYDSS 450
mEpithin --------GS --------S- --S----H-- --H------- ---------N

hTADG15  DPCPGQFTCR TGRCIRKELR CDGWADCTDH SDELNCSCDA GHQFTCKNKF 500
mEpithin -----M-M-K ---------- -------P-Y ---RY-R-N- T-------Q-

hTADG15  CKPLFWVCDS VNDCGDNSDE QGCSCPAQTF RCSNGKCLSK SQQCNGKDDC 550
mEpithin ---------- ------G--- E------GS- K-------PQ --K-----N-

hTADG15  GDGSDEASCP KVNVVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSDEK 600
mEpithin ---------D S----S---Y ----Q----- ---------- T---------

hTADG15  DCDCGLRSFT RQARVVGGTD ADEGEWPWQV SLHALGQGHI CGASLISPNW 650
mEpithin N--------- K--------N ---------- ---------L --------D-

hTADG15  LVSAAHCYID DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH 700
mEpithin -------FQ- -KN-K---Y- M-------L- --K---S--- -LK-----T-

hTADG15  PFFNDFTFDY DIALLELEKP AEYSSMVRPI CLPDASHVFP AGKAIWVTGW 750
mEpithin -S-------- ---------S V---TV---- -----T---- ----------

hTADG15  GHTQYGGTGA LILQKGEIRV INQTTCENLL PQQITPRMMC VGFLSGGVDS 800
mEpithin ---KE----- ---------- -------D-M ---------- ----------

hTADG15  CQGDSGGPLS SVEADGRIFQ AGVVSWGDGC AQRNKPGVYT RLPLFRDWIK 850
mEpithin ---------- -A-K---M-- -------E-- ---------- ---CSSGLDQ

hTADG15  ENTGV*(SEQ ID NO:2)                                      900
mEpithin RAHWGIAAWT DSRPQTPTGM PDMHTWIQER NTDDIYAVAS PPQHNPDCEL

hTADG15
mEpithin HP(SEQ ID NO:10)                                        902
```

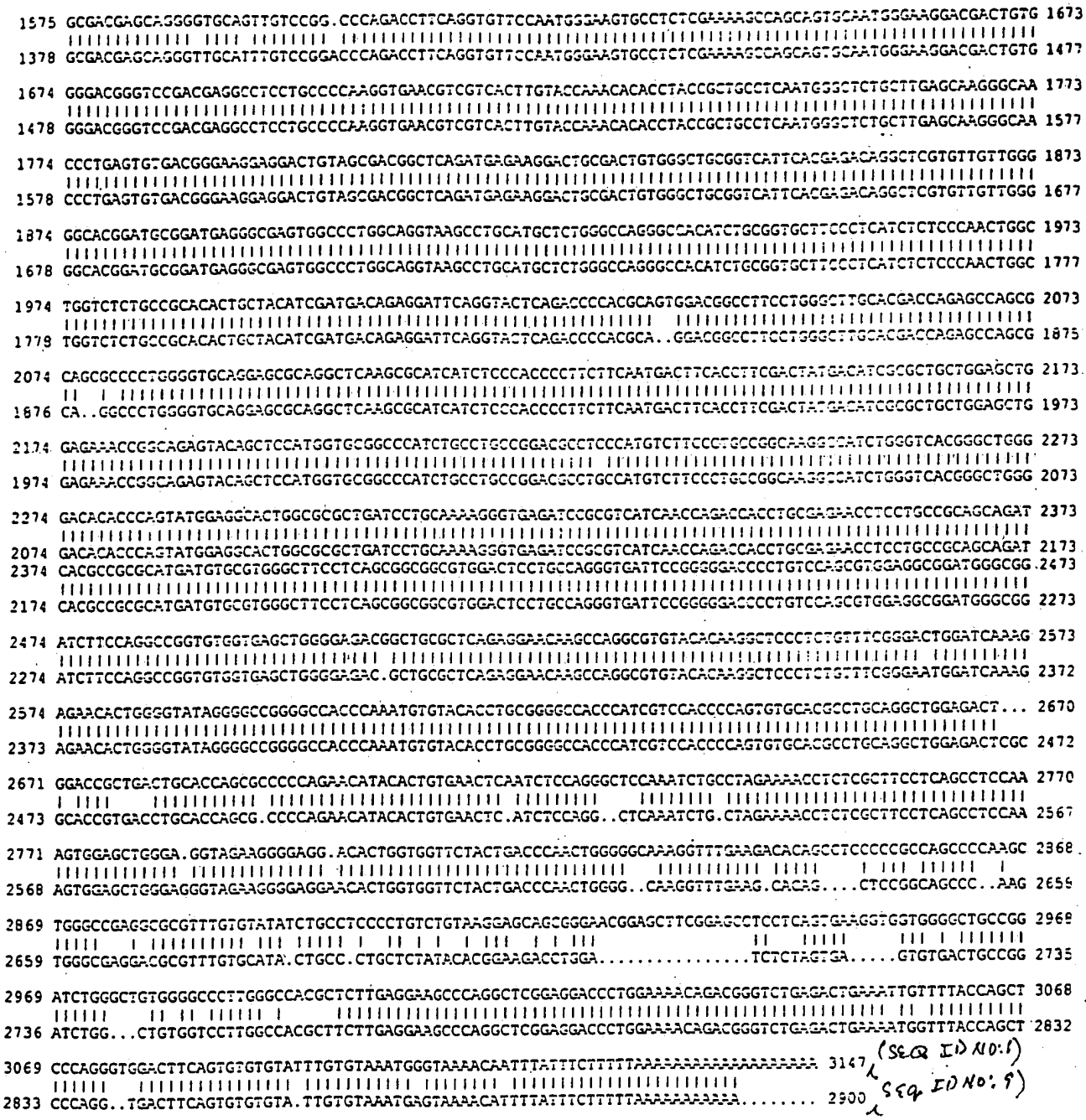
FIGURE 11

```
LOCUS       HSU20428     2900 bp    mRNA            PRI       17-MAR-1997
DEFINITION  Human SNC19 mRNA sequence.
ACCESSION   U20428
NID         g1890631
KEYWORDS    .
SOURCE      human.
ORGANISM  Homo sapiens
          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2900)
AUTHORS   Zheng,S., Cai,X., Geng,L., Cao,J., Zheng,L. and Zhi,Z.Z.
TITLE     SNC19 gene in Homo sapiens
JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2900)
AUTHORS   Zheng,S.
TITLE     Direct Submission
JOURNAL   Submitted (30-JAN-1995) Shu Zheng, Cancer Institute, Zhejiang
          Medical University, Hangzhou, 310009, Peoples Republic of China
```

```
TADG15: TCAAGAGCGGCCTCGGGGTACCATGGGGAGTGATCGGGCCTGCAAGGGCGGAGGGGGCCCCGAAGGACTTCGGCGCGGGACT 81

SNC19:  ..................................................................................

 82 CAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAAGGCGTGGAGTTCCTGCCAGTCAACGACGTCAAGAAGGTGGAAAAGCATGGCCCGGGG 181

    ..................................................................................

182 CGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCC 281
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1 CGCTGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCC 100

282 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAGCAAGGT 381
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
101 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTAAGCCTGGCCAGCAAGGT 200

382 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCTTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCC 481
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCTTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCC 300

482 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCCGAGGAGCGCGGTAGTCATGCTGCCCCCGCGGGCGCGCT 581
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTTGAGGAGGCCGAGCGCGTCATGGCC.AGGAGCGCGGTAGTCATGCTGCCCCCGCGGGCGCGCT 399

582 CCCTGAAGTCCTTTGTGGTCACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGCAGCTTTGGCCTGCACGC 681
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
400 CCCTGAAGTCCTTTGTGGTCACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGCAGCTTTGGCCTGCACG. 498

682 CCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCTGACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGAC 781
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
499 CCGCGGTGTGGAGCTGATGCGCTTCACCACG.CCGGCTTCCCTGACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGC....TGCGGGGACG.CGAC 592

782 TCAGTGCTGAGCCTCACCTTC.....CGCAGCTTTGACCTTGCGTCCTCGACGAGCGCGGCAGCGACCTGGTGACGGTGTACAACACCCTGAGCCCCAT 876
    |||||||||||  | |   |     ||||| ||||   || |    ||||||||||||||||||||||||||||||||||||||||||||||||||
593 GCAGTGCTGAGCTACTCGAGCTGACTCGCAGC.TTGACTGCGCCT....CGACGAGCGCGGCAGCGACCTGGTGAC.GTGTACAACACCCTGAGCCCCAT 686

877 GGAGCCCCACGCCCTGGTGCAGTTGTGTGGCACCTACCCTCCCTCCTACAACCTGACCTTCCACT.CCTCCCA.GAACGTCCTGCTCATCACACTGATAA 974
    |||||||||||| |||||||    ||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||
687 GGAGCCCCACG.CCTGGTG..AGTGTGTGGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCCTCCCACGAACGTCCTGCTCATCACACTGATAA 783

975 CCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATT 1074
    |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
784 CCAACACTGA..CGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATT 881

1075 CAACAGCCCCTACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTGAGCTTCAAATTC 1174
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 682 CAACAGCCCCTACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAAAATTGAGGTGCCCAACAACCAGCATGTGAAGGTGCGCTTCAAATTC 981

1175 TTCTACCTGCTGGAGCCCGGCGTGCCTGCGGGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCG 1274
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 982 TTCTACCTGCTGGAGCCCGGCGTGCCTGCGGGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCG 1081

1275 TCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCTACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGA 1374
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1082 TCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCTACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGA 1161

1375 CCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGGCCGACTGCACCGACCACAGCGATGAGCTC 1474
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1162 CCCATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGG.CGACTGCACCGACCACAGCGATGAGCTC 1260

1475 AACTGCAGTTGCGACGCCGGCCACCAGTTCACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACA 1574
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 AACTGCAGTTGCGACGCCGGCCACCAGTTCACGTGCAAGAGCAAGTTCTGCAAG...CTCTTCTGGGTCTGCGACAGTGTGAACGAGTGCGGAGACAACA 1377
```

FIGURE 12

C



(SEQ ID NO:1)

(SEQ ID NO:9)

12 (Continued)

FIGURE 12-2